

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.  
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
15 (C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/430035  
(B) FILING DATE: 27-Apr-1995  
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/196689  
(B) FILING DATE: 15-FEB-1994

35 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/185607  
(B) FILING DATE: 21-JAN-1994

40 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/176553  
(B) FILING DATE: 03-JAN-1994

45 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Winter, Daryl B.  
(B) REGISTRATION NUMBER: 32,637  
(C) REFERENCE/DOCKET NUMBER: P0871P2D2

50 (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415/225-1249  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu  
-16 -15 -10 -5

15 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
1 5 10

15 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
15 20 25 26

20 (2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 GAATTCCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

35 CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91  
Leu Leu Leu Val Val Met Leu  
-16 -15 -10

40 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130  
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro  
-5 1

45 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169  
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg  
5 10 15

45 GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210  
Asp Ser His Val Leu His Ser Arg Leu  
20 25 26

50 CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260

50 GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310

50 TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 TCTAGACGAG AGCTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50  
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100  
GGTCAAGGAG TTAGAGGAAG TGATGGTGTGTC TTCCTGGGAG TATGGGTGTC 150  
20 TTACCAAGTTA CGCGGATAAAA GGGGATAATG TTGGGAGTTTC TCACCAGTCT 200  
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250  
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300  
25 AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350  
ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATT 390

30 (2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 353 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr  
-21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu  
-5 1 5

45 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser  
10 15 20

Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
25 30 35

50 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
40 45 50

Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu  
55 60 65

5 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu  
85 90 95

10 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro  
100 105 110

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu  
115 120 125

15 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
130 135 140

20 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr  
145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu  
160 165 170

25 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser  
175 180 185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe  
190 195 200

30 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
205 210 215

35 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn  
220 225 230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly  
235 240 245

40 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro  
250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro  
265 270 275

45 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr  
280 285 290

50 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro  
295 300 305

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His

310

315

320

Ser Gln Asn Leu Ser Gln Glu Gly  
325 330 332

5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1798 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15

GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50  
GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCCT TGGCCCGCCT 100  
20 TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150  
GGCCCCAGGA AGGATTCAAGG GGAGAGGCC CAAACAGGGA GCCACGCCAG 200  
25 CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242  
Met Glu Leu Thr Glu Leu Leu Leu  
-21 -20 -15

30

GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281  
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser  
-10 -5

35

AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320  
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser  
1 5 10

40

AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359  
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
15 20 25

AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398  
Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
30 35

45

CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437  
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys  
40 45 50

50

ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 476  
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly  
55 60 65

	GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 515		
	Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg		
	70	75	
5	GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 554		
	Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly		
	80	85	90
10	CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 593		
	Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu		
	95	100	
15	CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 632		
	Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg		
	105	110	115
20	ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 671		
	Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser		
	120	125	130
25	TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 710		
	Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met		
	135	140	
30	CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 749		
	Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro		
	145	150	155
35	CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 788		
	Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu		
	160	165	
40	ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 827		
	Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu		
	170	175	180
45	GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 866		
	Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser		
	185	190	195
50	GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 905		
	Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile		
	200	205	
55	CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 944		
	Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln		
	210	215	220
60	ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 983		
	Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn		
	225	230	

1022  
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr  
235 240 245

1061  
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr  
250 255 260

1100  
Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro  
265 270

1139  
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe  
275 280 285

1178  
Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
290 295

1217  
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr  
300 305 310

1256  
Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser  
315 320 325

1300  
CAG AAT CTG TCT CAG GAA GGG TAA GGTTCTCAGA CACTGCCGAC  
30 Gln Asn Leu Ser Gln Glu Gly  
330 332

1350  
ATCAGCATTG TCTCATGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA

1400  
GACAACCTGGA CAAGATTTC TACTTTCTCC TGAAACCCAA AGCCCTGGTA

1450  
AAAGGGATAC ACAGGACTGA AAAGGGATC ATTTTCACT GTACATTATA

1500  
AACCTTCAGA AGCTATTTT TTAAGCTATC AGCAATACTC ATCAGAGCAG

1550  
CTAGCTCTT GGTCTATTTT CTGCAGAAAT TTGCAACTCA CTGATTCTCT

1600  
ACATGCTCTT TTTCTGTGAT AACTCTGCAA AGGCCTGGGC TGGCCTGGCA

1650  
GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAGGGTA

1700  
ATTTCCCTTG CTTCAAATTC AAGGCCTTCC AACGCCCCCA TCCCCTTTAC

1750  
TATCATTCTC AGTGGGACTC TGATCCCATA TTCTTAACAG ATCTTTACTC

1798  
TTGAGAAATG AATAAGCTTT CTCTCAGAAA AAAAAAAA AAAAAAAA

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1798 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTT TCTGAGAGAA AGCTTATTCA TTTCTCAAGA 50  
15 GTAAAGATCT GTTAAGAATA TGGGATCAGA GTCCCACTGA GAATGATAGT 100  
AAAGGGATG GGGGCGTTGG AAGGCCTTGA ATTGAGAGCA AAGGAAATTA 150  
20 CCCTTTCTCT GTTTTCTGAC TCAAGGTTAG TCTCTCCCTC TGTTCAACTG 200  
CCAGGCCAGC CCAGGCCTTT GCAGAGTTAT CACAGAAAAA GAGCATGTAG 250  
AGAATCAGTG AGTTGCAAAT TTCTGCAGAA AATAGACCAA AGAGCTAGCT 300  
25 GCTCTGATGA GTATTGCTGA TAGCTTAAAA AAATAGCTTC TGAAGGTTA 350  
TAATGTACAG TGAAAAATGA TTCCCTTTTC AGTCCTGTGT ATCCCTTTA 400  
CCAGGGCTTT GGGTTTCAGG AGAAAGTAGG AAATCTTGTG CAGTTGTCTC 450  
30 CCAGGGCGC CCTGCAGGGGA AGGGAGCTGT ACATGAGACA ATGCTGATGT 500  
CGGCAGTGTC TGAGAACCTT ACCCTTCCTG AGACAGATTC TGGGAGTGGG 550  
TGTAGGATGT GTTTAGAAGA GGGCTGGTAG GGGTGGCGT TGGAGCAGAA 600  
35 GGGTCAGGAA GCAGGGGGTG GAGCTGGACC ACAGGGGTGG GCAAGGTGGG 650  
TGGAAGAGGG AAGAGCGTAT ACTGTCCAGT AGGAGGATGG GTTGGGAAG 700  
40 GAGAATATCC AGGCTGGAGG TTGGGTGGCA GGGAGCCTGT GTCTGATGTT 750  
CCTGAGGAAA TGTCCGGGGC TCCTAGGGTC CTGCGTGAGG GTCCAGGAAA 800  
GAGTCCACGA GTTCCATTCA AGAGTCGTG TATCCTGTTC AGGTATCCGG 850  
45 GGATTTGGTC CAGGGACCTG GAGGTTGGT TCAGCAGACC AGGAATCTTG 900  
GCTCTGAATC CCTGCTGCCA CTTCAGAAGC CCAGAGCCAG TAGTTCTGGC 950  
50 TGAGGCAGTG AAGTTGTCT CCAACAATCC AGAAGTCCTG TTTGGGAGCT 1000  
CGTTCACTGT GAGGACTAGA GAGGTTCTGC TGGGGACAGC TGTGGTGGGT 1050

GGGGCCCGCC TGACGCAGAG GGTGGACCCT CCTACAAGCA TCAGGAAACG 1100  
CACCTTCCT CGGAGCAGGT GTTGGAAAGCT CAGGAAGATG GCATTGGGAT 1150  
5 CCTTGTGAGC TGTGGTCCTG CCCTGTGGAG GAAGCTGGGT TCCAAGGAGG 1200  
CTCTGCAGGG CCCCAAGGAG GAGACGGACC TGTCCAGAAA GCTGCCAG 1250  
GAGGGATGAG AGGCAAGTGG GTCCCAGTTG TCCCCGTGCT GCCATCACTC 1300  
10 CCTCCAGCAG AAGGGTCACT GCTCCCAGAA TGTCCGTGCT CTTGGTCTCC 1350  
TCCATCTGGG TTTTCCATTG TCCCAAGCTA AAGTCCACAG CAGGCAGCAG 1400  
15 GACAGGTGTA GGCAAAGGGT GAACCTCTGG GCACTGGCTC AGTCTGCTGT 1450  
GAAGGACATG GGAGTCACGA AGCAGTTAC TGAGGACTCG GAGGTCACAA 1500  
20 GCAGGAGGAG CCGGGCTGGA CAGCGTTAGC CTTGCAGTTA GGAGAACAT 1550  
GACCACGAGG AGCAATTCAAG TCAGCTCCAT TCTGGCCGGG GTGTCTGGCT 1600  
GGCGTGGCTC CCTGTTGGG GCCTCTCCCC TGAATCCTTC CTGGGGCCAT 1650  
25 GGAGGCGGCT TAGGCTCTTG CACTTCTGGG CAGAGTAGGG TGGGGCAAAG 1700  
GCGGGCCAAG GGTGAGGAAT CTATCCGGGT GGAGAACGGC TCCAGGACCC 1750  
AAGTGCACAG CAGGCAGCCC TCTGGGGAGC AGATGGGTAG GAAGACGC 1798  
30 (2) INFORMATION FOR SEQ ID NO:7:  
      (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 193 amino acids  
35          (B) TYPE: Amino Acid  
          (D) TOPOLOGY: Linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser  
      1                  5                  10                  15  
Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro  
      20                  25                  30  
45 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu  
      35                  40                  45  
50 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys  
      50                  55                  60  
Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe

	65	70	75
	Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val		
	80	85	90
5	Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln		
	95	100	105
10	Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu		
	110	115	120
	His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu		
	125	130	135
15	Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp		
	140	145	150
20	Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe		
	155	160	165
	Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu		
	170	175	180
25	Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg		
	185	190	193

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu			
1	5	10	15
Leu Arg Asp Asp His Val Leu His Gly Arg			
20		25	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu			
1	5	10	15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
20 25 26

5 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15  
15 Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu  
20 25 26

20 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15  
30 Leu Arg Asp Asp His Val Leu His Gly Arg  
20 25

35 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys  
1 5 10 14

45 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5           GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:14:

10           (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 20 base pairs  
              (B) TYPE: Nucleic Acid  
              (C) STRANDEDNESS: Single  
              (D) TOPOLOGY: Linear

15           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCNGCNCCNC CNGCNTGYGA 20

20           (2) INFORMATION FOR SEQ ID NO:15:

25           (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 21 base pairs  
              (B) TYPE: Nucleic Acid  
              (C) STRANDEDNESS: Single  
              (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30           NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:16:

35           (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 69 base pairs  
              (B) TYPE: Nucleic Acid  
              (C) STRANDEDNESS: Double  
              (D) TOPOLOGY: Linear

40           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

45           TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:17:

50           (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 69 base pairs  
              (B) TYPE: Nucleic Acid  
              (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 CCAGCACCTC CGGCATGTGA CCCCGACTC CTAAATAAAC TGCTTCGTGA 50  
CGACCACGTC CATCACGGC 69

10 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
15 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20 Pro Arg Leu Leu Asn Lys Leu Leu Arg  
1 5 9

(2) INFORMATION FOR SEQ ID NO:19:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCGC CGGCATGTGA CCCCGACTC CTAAATAAAC TGCTTCGTGA 50  
35 CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:20:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

50 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGTCTGCCG TGAAGGACAT GG 22

10